GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 9, 2000, 09:57:10 ; Search time 1721.35 Seconds
                                            (without alignments)
                                            13243.098 Million cell updates/sec

Title:
Perfect score: 3687
Sequence: 1 atggataggaaaaagctgt...............ttacattctatattaagtaa 3687

Scoring table: IDENTITY.NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 309140324 3 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
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23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
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62: em_esthum20:*
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65: em_estin3:*
66: em_estin4:*
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69: em_estov2:*
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76: em_estro2:*
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86: em_estro12:*
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91: gb_gss4:*
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93: gb_gss2:*
94: em_gss3:*
95: em_gss4:*
96: em_gss5:*
97: gb_gss6:*
98: gb_gss7:*
99: gb_gss8:*
100: gb_gss9:*
101: em_gss5:*
102: em_gss6:*
103: em_gss7:*
104: em_gss8:*
105: em_gss9:*
106: em_gss10:*
107: em_gss11:*
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109: gb_gss11:*
110: gb_gss12:*
111: em_gss12:*
112: gb_gss13:*
113: gb_gss14:*
114: gb_gss15:*
115: gb_gss16:*
116: gb_gss17:*

RESULT   1
CNS0134P/c

```
117: gb_gss18:*
118: gb_gss19:*
119: em_gss13:*
120: gb_gss20:*
121: gb_gss21:*
122: gb_gss22:*
123: gb_gss23:*
124: em_gss14:*
125: em_gss24:*
126: gb_gss15:*
127: em_gss16:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	59.8	1.6	997	121	CNS0134P	AL102403 Drosophil
2	56.4	1.5	476	34	BE224646	BE224646 kp59a06.y
3	55.8	1.5	1159	121	CNS015XR	AL106041 Drosophil
4	55.8	1.5	773	122	CNS01VTG	AL165549 Tetraodon
5	55.2	1.5	735	123	CNS04NSM	AL299119 Tetraodon
6	55.2	1.5	917	121	CNS017SL	AL108447 Drosophil
7	54.2	1.5	1076	124	CNS05HXN	AL331180 Tetraodon
8	53.4	1.5	560	121	CNS00CI3	AL059106 Drosophil
9	53.4	1.4	1101	121	CNS01807	AL108721 Drosophil
10	53	1.4	1025	121	CNS014J2	AL104216 Drosophil
11	53	1.4	1147	118	B13042	B13042 T30M24-Sp6.
12	51.8	1.4	959	121	CNS00655	AL062806 Drosophil
13	51.8	1.4	969	121	CNS00IDL	AL074848 Drosophil
14	51.8	1.4	1101	121	CNS00HX9	AL073856 Drosophil
15	51.6	1.4	470	124	FR0018463	AL011359 F.rubripe
16	51	1.4	1042	121	CNS0148K	AL103838 Drosophil
17	51	1.4	1184	123	CNS01807	AL308050 Tetraodon
18	50.8	1.4	1101	121	CNS04P4P	AL063921 Drosophil
19	50.8	1.4	539	21	CNS0039G	AW329517 N20762e
20	50.6	1.4	1101	121	CNS00EVL	AL069706 Drosophil
21	50.6	1.4	989	122	CNS02HA4	AL197365 Tetraodon
22	49.6	1.3	828	121	CNS011TX	AL100719 Drosophil
23	49.6	1.3	581	122	CNS034DX	AL227297 Tetraodon
24	49.2	1.3	809	121	CNS00A7H	AL054820 Drosophil
25	49	1.3	869	121	CNS002EK	AL097574 Drosophil
26	49	1.3	1223	118	B12981	B12981 T24D11-Sp6
27	48.8	1.3	1079	122	CNS035IX	AL228786 Tetraodon
28	48.8	1.3	1007	121	CNS00JOV	AL076752 Drosophil
29	48.8	1.3	421	115	AZ113646	AZ113646 RPCI-23-4
30	48.4	1.3	443	124	FR0008252	Z92062 F.rubripes
31	48.4	1.3	450	124	CNS001FB	AL018519 F.rubripe
32	48.4	1.3	1101	124	CNS001FB	AL060732 Drosophil
33	48.2	1.3	567	124	FR0006951	Z90761 F.rubripes
34	48	1.3	426	14	AL366543	AL366543 MtBA08F06
35	48	1.3	500	20	AW126318	N100425e
36	48	1.3	518	34	BE239628	EST403677
37	47.8	1.3	907	122	CNS021J4	AL176953 Tetraodon
38	47.8	1.3	1101	122	CNS0182P	AL108811 Drosophil
39	47.6	1.3	945	121	CNS006WN	AL066018 Drosophil
40	47.4	1.3	838	123	CNS03W9J	AL263440 Tetraodon
41	47.2	1.3	767	121	CNS00AQX	AL055924 Drosophil
42	47.2	1.3	783	121	CNS00AIS	AL055833 Drosophil
43	47.2	1.3	823	121	CNS0105K	AL098546 Drosophil
44	47.2	1.3	894	34	BE215316	BE215316 HV_CEb000
45	47.2	1.3	1152	122	CNS024NL	AL181002 Tetraodon

ALIGNMENTS

```
LOCUS       CNS0134P     997 bp    DNA             GSS       26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN09C07 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL102403
VERSION     AL102403.1  GI:5614014
KEYWORDS    GSS.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 997)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage ;
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
COMMENT     - Web : www.genoscope.cns.fr)
            Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebl.ac.uk .. This Drosophila Genome melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES             Location/Qualifiers
     source          1..997
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN09C07"
                     /note="end : SP6"
BASE COUNT      162 a    115 c     79 g    517 t    124 others
ORIGIN
```

```
Query Match        1.6%;    Score 59.8;    DB 121;    Length 997;
Best Local Similarity  37.5%;    Pred. No. 0.0015;
Matches  245;   Conservative  43;   Mismatches 362;   Indels  3;   Gaps  1;
```

```
Qy    437 aagcaaaagatttagaaaaagcagaaacaatactatccacaaaattccttatgaaattaaa 496
              ||:| | |||||| | |||| ||  | |:  |  || |||||| |:||  |||||
Db    656 AAAAAAAWAAAAAAAAAAAATAAAAAAAAAAATAAAAGAAAAGAARTTAGAGAAWAAAAT  597

Qy    497 ctcgcacagtcatttagatcgcgtatatggtaaaacaactcgtgattacttcgctcta   556
              :||  | | ||||||  |||| | |||| | ||||  || |||  |||| ||| |
Db    596 ATTAAAAAGAAATAAATAAAAAAAAWGAAAGRAGAAARAAAAGGAAAAWAWAAAAAA    537

Qy    557 catttaaagcaaagcacaagagaacttcgcgacagcttaatttatgatattaccgttgcaa 616
              |||||| | ||| ||  ||| |||  | ||  | || |||| ||  |:| |  ||
Db    536 WAAWAAWAAAAWRAAAWRTAAAAAAGRATAWAAAAARTRAAAAGAAAWWAAWAAAAAGWAA  477

Qy    617 tgaaagcgcgcgaagtaccaagacgctgtgaaagcgcaattagacaaagctaaagctg    675
              ||  | | | || | ||| |||  | ||  | ||| ||||| ||| ||||||  ||:
Db    476 AATAAAAAWATAAAACAAAAAAAAGATAAAAAAAWGAAAAAAAAAWGAAAATAAAAAWAAAA 417

Qy    677 ctgttgatcaaatcaatacattaccaaaagtaacacagaatgcttcaaaactgaactaa   736
              | |||| | ||  | || |||  ||| ||  | || |||| | |||  ||| ||||
Db    416 WTGAWAAAAGAGAAAAAAAAATAATATATWTAAAATAAAATTAGWAGRATARATAAWTGAAAATAA 357

Qy    737 cagaagtagcgaaaaagcattagatgcgagatgaagctcgcgcttacctccaaaagttgaa 796
              | ||| | ||  ||||| || || ||  || ||||| || ||  ||||  |||| ||||
Db    356 AAGAAAAAAAAAAAAAAAATWAAAAAWRAAAAAACATAATWRGWGTAAAACAAAAAAGGAAAAA 297

Qy    797 gtgtaagtcgcgattaacactcaaaacaaagctgttgaattaacagcagtacagtgaacg   856
              || ||| | | |||  ||| | |||  |||| ||| |||| ||| ||| ||  ||
Db    296 AAAARAAAAAAWAWAAAAGARAAAAAAAAAAANNNNNANNNNNNNNNAAANNNNNNAANNNN   237

Qy    857 gaacaactaaaaattacacacttcagctgctgcaaatgaagatacagtaaacgtaaatactg 916
              | |  |||  | ||  || |  ||| || |  |||| || |||| ||| ||   |||| ||
Db    236 NNGANNNANNNAAAANATGTTRCAAATWAWAAGTATRGAAAAAAAAAATAARWAAAAAA---  178
```

```
Qy   917 tacgtatcattaaagtggacggtaacattccattgccccttaatacggcagatgttctt 976
         ::|.:||| .|||  |||.| ::|  :| ||  ||||:|      | |||   |
Db   179 ARARAAAGWARAAAAWARWTWTCCAAAGAGAGAGAGTTTAWAAGTTAWAGACATGAMC 120

Qy   977 tatctacagacggaaaactatcactgtggatgtcttcaactccattcgaaatataccg 1036
Db   119 TTAGCAATAAGGWAATRAAAAAAWTAAAAAGTTWTACAAAAAAGGTAAWWTAA 60

Qy  1037 agtataaagtaagttaaaggtattaaagacgacaaaaatggcaaaaaatttaaa 1089
Db    59 ACCGGAAACAAGTTGTAAAAAAATGAAAAAAAAAATTATTMGWATTGWAATRAAM 7
```

RESULT   2

LOCUS   BE224646   476 bp   mRNA   EST   06-JUL-2000
DEFINITION kp59a06.y1 TBN95TM-SSFH Strongyloides stercoralis cDNA 5' similar
            to TR:046362 046362 HISTONE 1. [4] TR:046140 TR:046142 TR:046142
            ;contains element MER31 repetitive element ;, mRNA sequence.
ACCESSION   BE224646
VERSION   BE224646.1 GI:8929882
KEYWORDS   EST.
SOURCE   Strongyloides stercoralis.
  ORGANISM Strongyloides stercoralis
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
            Panagrolaimoidea; Strongyloididae; Strongyloides.
REFERENCE   1 (bases 1 to 476)
  AUTHORS   McCarter,J., Clifton,S., Maira,M., Hillier,L., Kucaba,T., Martin,J.
            , Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen
            ,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey
            ,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas
            ,M., McCann,R., Waterston,R. and Wilson,R.
  TITLE   The Washington Univ. Nematode EST Project, 1999
  JOURNAL   Unpublished (1999)
COMMENT   Contact: McCarter JP
            Email: est@watson.wustl.edu
            The library was constructed by Dr. Thomas Nutman and colleagues of
            NIAID, NIH (tnutman@nih.gov). DNA Sequencing by: Washington
            University Genome Sequencing Center St. Louis.
            Seq primer: -40RP from Gibco
            High quality sequence stop: 435.
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu

FEATURES   Location/Qualifiers
     source   1..476
                     /organism="Strongyloides stercoralis"
                     /strain="Filariform larvae obtained from humans"
                     /db_xref="taxon:6248"
                     /clone_lib="TBN95TM-SSFH"
                     /lab_host="XL-1 Blue MRF' (Stratagene)"
                     /note="Vector: Lambda Uni-ZAP XR (Stratagene); Site_1:
                     EcoRI; Site_2: XhoI; mRNA was purified from 4 x 10E5
                     filariform larvae which had been isolated from infected
                     humans. cDNA was constructed and, using adaptors, was
                     cloned unidirectionally into the vector from the EcoRI
                     site to the XhoI site. The library has an unamplified
                     titer of 1.5 x 10E6 pfu/ml and an amplified, undiluted
                     titer of 7 x 10E9 pfu/ml. The average insert size of the
                     unamplifed library is 975 bp (range, 500-1500)."

BASE COUNT   218 a   72 c   72 g   114 t
ORIGIN

Query Match   1.5%; Score 56.4; DB 34; Length 476;
Best Local Similarity 52.68%;
Matches 123; Conservative   0; Mismatches 111; Indels   0; Gaps   0;
Pred. No. 0.0076;

```
Db   218 AAACCAAGTGGCGGATAAGAAAAAGTTGTCAAAAAAACAGTTGCCAAAAAAGCTGTAGACACT 277
Qy  1651 gaaaaagaatctggtacagttggtgttctctgaactaaaataataatgcagaccgctaaatg 1710
Db   278 AAAAAACGAACTGATTCAAAAGAAGAAGCTRACTGAWGTCAAAAAAACTTCGATGTTAAAAA 337
Qy  1711 gtaacttagtgccaaagacggagacccttaaaagaaaatacaatctatcaaaatcaaattaaa 1770
Db   338 ACAACTAAGTCTCCAAAAAGCTRAGACTACAGAAAAAAAGTCTTGAAAAAAACAAATTGAA 397
Qy  1771 aaaggcttgaagtccgataaagatgtattagtcgacactgttaacgcaggcgagcaaaaca 1824
Db   398 AAGAGAACAAAAATCTACTCCTACAAAAGACAAGTAGCCACAAAAGTTGCTAAAAA 451
```

RESULT   3

LOCUS   CNS015XR   1159 bp   DNA   GSS   26-JUL-1999
DEFINITION CNS015XR.
            Drosophila melanogaster genome survey sequence T7 end of BAC
            BACN15017 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL106041
VERSION   AL106041.1 GI:5619746
KEYWORDS   GSS.
SOURCE   fruit fly.
  ORGANISM Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 1159)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT   Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.

FEATURES   Location/Qualifiers
     source   1..1159
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN15017"
                     /note="end : T7"

BASE COUNT   448 a   36 c   7 g   178 t   490 others
ORIGIN

Query Match   1.5%; Score 55.8; DB 121; Length 1159;
Best Local Similarity 33.8%;
Matches 189; Conservative   6; Mismatches 365; Indels   0; Gaps   0;
Pred. No. 0.013;

```
Qy   212 aatacacaaatgcgaaaaaacgataccgtgatgcggtagcattagtgaataaagcaggtg 271
Db    31 AAAAAAAAAAAAAAAYAAAAAAMSAMAAAAAAAHNCYAAAAAAAAAAAAAA 90
Qy   272 gcgcgaaaaa3gacgcgttacttagctgattacaaaagaatatgaaacttacgtttca 331
Db    91 AACAAAAAAANAAAAAAANNANTNTNTNNATTNTATANAAAAAAAAAAAAAAAAA 150
Qy   332 aagcaaacctaaatctggcgaagctcgtgtagcaacttacatcgatgctcacaactatg 391
Db   151 AAAAAAACNCACACCCAACNNAAMCCCAAAMACCAANCNNNNNANNANAANNNNAAANNN 210
Qy   392 caacaaaattagacgaaatgcgccaagagctgaggcgctgttcaagcaaaagatttag 451
```

```
Qy  1591 acaacaacgttgctactaaggttagacgaatctactttagctgataaactttgtattagtt 1650
```

```
Db    211 NAAAAAACNNANANANANANANANNANNTAAAAANANANAAAAAAAAAAAAA 270
Db    452 aaaagcagaacaatactatcacacaaaattccttatgaaattaaaactgcaacagtcatt 511
          ||||||  ||| ||   |   ||| |||| | | ||  ||| ||
Db    271 AAAAAAAAAAAAAAAAANAANNNNANNNNNANNAAANNANNNNAAAAANNANAAACAAAAA 330
Qy    512 tagatccgtatatggtaaaacaactcgtgattacttcgctctacatttaaagcaaaag 571
          |||||| | |||||||||  || | |||||||||||  ::| |||||||  :||
Db    331 NAANNNAAAAAANNANNNNNNNANANBCANADTTWTTTAAANNAAANANAAAAAYANNN 390
Qy    572 cacagagaacttcgccgacagcttaattatgatattaccgttgcaatgagaaagccgcgcaag 631
          ||:||  |:|  |   |||  | |  ||||  ||  ||  ||||  |||| |||| |||| |||
Db    391 NNNAAAAAANNNNANNNNNNNANANNAAAAANNNAAAAAAANNNAAAANANNNA 450
Qy    632 tacaagacgctgtgaaagcaggcaatttagacaaagctaaagctgtcgtttgatcaaatca 691
          | || ||||  | |  |||  ||  |||  |  |||||||  || ||| |  | ||| |
Db    451 ANNAANNNNANNNNNAAANNNNNANNNNANNNNNNAANNNANNNAAAAAANNNA 510
Qy    692 atcaatacttaccaaaaagtaacagatgcttcaaaactgaactacacagaagtagcgaaaa 751
          | |||| | || ||  |||  |||||||| |  ||||||  ||  || || ||||  ||||
Db    511 AAAAAAAAAAAAAAANNAAAAAAAAAAAAAANNNAAAAAAAAAAAAAAAAAAAAA 570
Qy    752 aagcattaagatgcaagatgaa 771
          || || ||| || | ||
Db    571 AAAAAAAAAAAAAAAAAA 590
```

```
RESULT 4
LOCUS       CNS01VTG                773 bp    DNA    GSS    12-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            199C24 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL169549
VERSION     AL169549.1  GI:7807606
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Euryptergii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
            Holacanthopterygii; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 773)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bonneau,L., Billault,A., Quetier,F., Saurin,W. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater puferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 773)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 773)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
            Genoscope.
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1..773
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="199C24"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0AG199BB12LP1-end : T7"
BASE COUNT      210 a    265 c    69 g   184 t    45 others
```

```
ORIGIN

Query Match     1.58;    Score 55.4;  DB 122;  Length 773;
Best Local Similarity   39.8%;  Pred. No. 0.015;
Matches 206;  Conservative 30;  Mismatches 281;  Indels 0;  Gaps 0;

Qy   1098 attcaacttcaagcttcgaaatgatgctgtagttacttcaagtgtttggaactaatgtaac 1157
          |||||||| || | |||| ||  ||| | |||||| || |||||||||| || ||  ::|
Db    122 ATCCAAYGTCTTGCATCAYATGGTTAATTTTTTATTTATTTACTCATGATGATACTGCTACTACTACWAC 181
Qy   1158 aaacacacttctgtaaacttagcacgcaggtacttcgaacctgacactgacgatactttaacagt 1217
          |  ||||| || ||||| |||||||  ||||  ||| |||| || || ||||| |||| |||
Db    182 TGCTACWACTACTGCWACWACWACCTACTGCWACTACTGCTACTACTGCTACTACTGC 241
Qy   1218 agtatttgataagttgttagcacctgaaactgtaaacgcttactattacga 1277
          |:|    ||  ||   ||  |  ||  ||||  | ||  ||  |||| ||| ||
Db    242 TACTGCTACTACTCTGCTACTACWAGTGCTACTACTACATGCWACTAC 301
Qy   1278 tgttgaaactggaaaacgcaattcccagtaattgcatctacttctggttctacaatttacat 1337
          ||:|  || ||||||| ||| ||  || |||  | |||| |||| ||| |||| |||| |||
Db    302 TGCWACTGCTACTACTACWACTACWACWACTGCTACTACTACTACTGCTACTACTAC 361
Qy   1338 tacgttaaagaaagcgttagtaactggtaaacaaatataaaactgtcatcaataagttaa 1397
          |: |     ||  ||  ||  ||  ||  ||  | ||  ||  || :||:||  |
Db    362 TGCAWACCAGCAPACACANTACTACTACTACATGCTACTACTACATACGCAACTACWGCAAC 421
Qy   1398 aacaattaactggttacaatgcagaagcttacgagttagttcaactgaaacgcatcagc 1457
          || ||||  | |||||||| |  ||| || || |:|||| |||  ||:|| |::||:||
Db    422 TGCWACYRCTCAGGWGWACTACTACCACGWACAACAACTACWRCWACTACWCTACTGCTAC 481
Qy   1458 accaactgttgctacggctcctactacttaggtggtacaaacttatctactggttctct 1517
          || |||| |||  || ||||  || || ||||:||||||| || ||||||||  |||
Db    482 AACTACTACTRCWACTGCTACTACTACTACTGCTACTACTACTACTACTACTACTACWGC 541
Qy   1518 tacaacaaaatgtttggggtaaattggctgtggttgttgaatgaagcggaacttatatcc 1577
          ||:|| |  ||   |||||||| |||||| || || || || ||||  ||||  ||||| |
Db    542 TACWACTACWACCTACTACTGCTACTRCAAACTGCTACTACWACTGCTACWACTCCWACTGC 601
Qy   1578 tggtcttcaattcacacacaacgtttgctactaagtta 1614
          | |  ||  |:|: ||  |:| ||  || |  ||  |  ||
Db    602 TACAACTACAACTACTACTACTACTRCAACTRCATACATRCTA 638
```

```
RESULT 5
LOCUS       CNS04NSM                735 bp    DNA    GSS    21-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            123M05 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL299119
VERSION     AL299119.1  GI:8038260
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Euryptergii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
            Holacanthopterygii; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater puferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 735)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
```

JOURNAL   Unpublished
REFERENCE   3 (bases 1 to 735)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
            Genoscope.
COMMENT   This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES   Location/Qualifiers
     source   1..735
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="123M05"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG123AG03LP1-end : T7"
BASE COUNT   242 a   45 c   223 g   197 t   28 others
ORIGIN

Query Match   1.58;   Score 55.2;   DB 123;   Length 735;
Best Local Similarity   45.7%;   Pred. No. 0.016;
Matches 168;   Conservative   6;   Mismatches 194;   Indels   0;   Gaps   0;

Qy   1241 ctgaaacctgtaaacaagctgaacgttactattacagaatgttgaacctggaaaacgcattc 1300
          || | || || | ||||| |
Db   534 CTACTACTGCTAAAACTACTACTGCTACTACTGCAGCTACTACTACTACTGCTACWATTK   475

Qy   1301 cagtaattgcatctacttcggttctacaattactacatctgttaaaagaacgttagtaa   1360
          | :| || || ||||||| ||||| ||||||||||||||||||||||
Db   474 CWGCTGCTACTACTACTACTACTACTACTACTACTGCTACTACTACTGCTGCTGCTA   415

Qy   1361 ctggtaaacaatataaacttgctatacataatgttaaaacattaactgttacaatgcag   1420
          |||| |||| | |||||||| | |||||
Db   414 CTACTGCTACTACTGCTACTACTGCTGCTACTACKGCKGCTGCTACTACTA   355

Qy   1421 aagttacgagttagtgttcactgcaaacgacatcagcacacaacgtgttgtaccgctccta 1480
          | |||| || | | | || ||||| | | |
Db   354 CTACTACTACTACTWTTWCTACTGCTACTACTACTACTGCTACTACTACTACTA   295

Qy   1481 ctacttaggtggtacaacttttatctactggttcttacacacaaaatgttttgggtaaat 1540
          || ||| |||| |||| |||| |
Db   294 CTACTACTACTACTRCTACTACTACTACTACTACTACTACTACTACTACTACTA   235

Qy   1541 tggctggtggtggaatggaagctggaaacttattatcctcggtcttcaattcaacaacagt 1600
          || || | || || | | || || || |||||||| || ||| | || ||
Db   234 CTGCTACCTGCTGCTACTACCACWACTACTACTACTACTACTACTACTACTACTACTACTA 175

Qy   1601 ttgctact 1608
          ||||||||
Db   174 CTGCTACT 167

RESULT 6
LOCUS   CNS017SL   917 bp   DNA   GSS   26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN37E22 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL108447
VERSION   AL108447.1 GI:5628751
KEYWORDS   GSS.
SOURCE   fruit fly.
  ORGANISM Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 917)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)

COMMENT   Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Geneviève Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES   Location/Qualifiers
     source   1..917
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN37E22"
                     /note="end : SP6"
BASE COUNT   174 a   132 c   51 g   410 t   150 others
ORIGIN

Query Match   1.58;   Score 55.2;   DB 121;   Length 917;
Best Local Similarity   39.3%;   Pred. No. 0.017;
Matches 125;   Conservative 39;   Mismatches 154;   Indels   0;   Gaps   0;

Qy   217 aacaaaagccgaaaaacgaataccgtgatgcgtagcattagtgaataaagcaggtggcgcg 276
          |::| | |||||||| | |: || || | | || | | |||
Db   471 AWAAMTTGGAAAAAWGRAAAAAATTGGTGTWRAGGATTACTKTTTTGGGCAGAAAAAAC   412

Qy   277 aaaaaagaacgcttacttagctgattacaaaaaagaatatgaaacttacgttttcaaagca 336
          |||| | || || |:||| | ||| ||| ||
Db   411 AAAAGCAAAAVAAMMAAAATATMAWWMWGAAARGRAAAAAWWWTWGGAANMAW   352

Qy   337 aaccctaaatctggcggaagctcgtgtagcaacttacatcgatgcttacaactatgcaaca 396
          ::| | |||| || | | | || | | ||| || | |
Db   351 WWACRCAWWTWTTGAAAGGAGGGGGGAGCAAMAAAWNATGCAAAAANAGACAAAAAAAW   292

Qy   397 aaattagacgaaatgcgccaagagctagaggcctgctgttcaagcaaaagattttagaaaa 456
          ||||| || |||| | ||||| | ||||| | || |||||||| |||| |||
Db   291 AAATTACMAWPAATGAACACAGATTGAAAGGAAAAWAWTATAACGAACAGWGAGGAAAR   232

Qy   457 gcagaacaatactatacacaaaattcctttatgaaattaaacctcgcacagtcatttagat 516
          | | ||||| | |:| | |||| |:   ::| || | |||| | | ||||:||
Db   231 AMATACMAAAWAMAGAMAAATAAAWWTTATAWGTWGTGRAAAAAAIGATAAWTTRATAA   172

Qy   517 cgcgtatatggttaaaaca 534
          | |:||| ||||||| |
Db   171 CCRAAATTGRAAAAAMA   154

RESULT 7
LOCUS   CNS05HXN   1076 bp   DNA   GSS   26-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T3 end of clone
            014F03 of library A from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL338180
VERSION   AL338180.1 GI:8231938
KEYWORDS   GSS; genome survey sequence.
SOURCE   Tetraodon nigroviridis
  ORGANISM Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
            Holacanthopterygii; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
REFERENCE   1 (bases 1 to 1076)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizanes,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE   Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   2 (bases 1 to 1076)

```
AUTHORS    Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
           Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
           Saurin,W. and Weissenbach,J.
TITLE      Human gene number estimate provided by genome wide analysis using
           Tetraodon nigroviridis DNA sequence
JOURNAL    Unpublished
REFERENCE  3  (bases 1 to 1076)
AUTHORS    Genoscope.
TITLE      Direct Submission
JOURNAL    Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT    This sequence is a single read and was generated as part of a large
           scale clone-end sequencing project of the Tetraodon nigroviridis
           genome. For more information, please take a look at
           http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1..1076
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone_lib="A"
                     /clone="014F03"
                     /note="Genoscope sequence ID : C0AA014CC02A1-end : T3"
BASE COUNT      160 a    260 c    309 g    333 t    14 others
ORIGIN

Query Match             1.5%;  Score 54.2;  DB 124;  Length 1076;
  Best Local Similarity   53.0%;
  Matches  116;  Conservative    0;  Mismatches  103;  Indels    0;  Gaps    0;

Qy       1463 ctgttgctaccgctcctactacttaggtggtgtacaacttatctactgttctcttacaa 1522
              |  ||||||||||||||||||||||||||||||||||||||||||
Db        793 CTGTCGGCTACTGTTGCTGCTCGTCACTGTTGTCGTCTGCTCACTGTTGCTGCTG 852

Qy       1523 caaatgttggggtaaattggctggtggtgtgaatgaagctggaacttattatcctggtc 1582
              |  |||
Db        853 CTACTGTTGCTGTGCTCGTCGCCTACTGTTGCTGCTCGTCACTGTTGCTGCTG 912

Qy       1583 ttcaattcacaacaacgtttgctactaagttagacgaaatctttacttttagctgataacttg 1642
              ||  | |||  |||
Db        913 TTGCTGTCGCTACTGTTGCTGCTCGTCACTGTTGCTGCTCGTCACTGTTGCTGCTACTG 972

Qy       1643 tattagttgaaaagaatctggtacaagttgttgttgcttcctg 1681
              ||  | |||
Db        973 TTGCTGTCGCTACTGTTGCTCGTCACTGTTGTCGTCCTG 1011


RESULT 8
CNS00Ci3
LOCUS       CNS00Ci3        560 bp    DNA        GSS       04-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence T7 end of BAC #
            BACR25J05 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL059106
VERSION     AL059106.1  GI:4946756
KEYWORDS    GSS.
SOURCE      fruit fly.
ORGANISM    Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 560)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
COMMENT     - Web : www.genoscope.cns.fr)
            Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
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COMMENT     Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp; the same strain used for the
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1..560
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR25J05"
                     /note="end : T7"
BASE COUNT      235 a    14 c    16 g    24 t    271 others
ORIGIN

Query Match             1.4%;  Score 53.4;  DB 121;  Length 560;
  Best Local Similarity   32.1%;
  Matches  120;  Conservative   12;  Mismatches  242;  Indels    0;  Gaps    0;

Qy        105 aacagtagtagccaagcaaaagcacagttcaaaaaagcatactacttacagccatac 164
              | |  | || |   |  |||  |
Db          2 AARAAAAARAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAANANANAAAAA 61

Qy        165 agtaacggaaactggtgaattcccaaacacattaacgatgtatatgctgaatacaacaaagc 224
              | |  |||   ||| |       |  || |||
Db         62 ANNNNNNNNNNAAAAAAAAAWAAAAWWAAAAAAAAANTAAAAAAANNAAAAAAAANNN 121

Qy        225 gaaaaacagataccgtgatgcggtagcacattagtgaataaaagcagggtggccgaaaaaga 284
              ||||  | |   || | |     | |||
Db        122 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAANWAGAAAAAATAATAAATATATAAWSADRATRWTAATRA 181

Qy        285 cgcttacttagctgatttacaaaaagaaatatgaaacttacgtttcaaagcaaacctaa 344
              |   |    | |   | |  |||
Db        182 GAAAAANTAAAAAANNCNAANNAAAAAAAAANNANNNANNNANANANNNNNANANANA 241

Qy        345 atctggcgaagctcgttgtagcaacttacatcgatgcttacaactatgcaacaaaattaga 404
              |     |   | |  |||
Db        242 NNAAANANNANAANNNANGNNNNNNNNAAANNNANNNTANNNGANNAANNNNNATNANNNNN 301

Qy        405 cgaaatgcgccaagagctagaggcgtctgttccaagcaaaagatttagaaaaagcagaaca 464
              | |  |     |  | |    |     |||
Db        302 NNAAAWAGNNNNNNNNAGNANGTGGCAATNGNNNNNAAANANAATNNNGNANANAAAAAATN 361

Qy        465 atactatcacaaa 478
              |   |    |||
Db        362 NANCAANNNNAAA 375


RESULT 9
CNS01807/c
LOCUS       CNS01807       1101 bp    DNA        GSS       26-JUL-1999
DEFINITION  Drosophila melanogaster genome survey sequence SP6 end of BAC
            BACN37F07 of DrosBAC library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL108721
VERSION     AL108721.1  GI:5629025
KEYWORDS    GSS.
SOURCE      fruit fly.
ORGANISM    Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
            Determination of this BAC-end sequence was carried out as part of a
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REFERENCE   1 (bases 1 to 1025)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage ;
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
  COMMENT   Determination of this BAC-end sequence was carried out as part of a
            collaboration with the European Drosophila Genome Project (EDGP) -
            http://www.edgp.ebl.ac.uk - ". This Drosophila melanogaster BAC
            library (Dros BAC) was made by Alain Billaud at CEPH (Centre
            d'Etude du Polymorphisme Humain) with funding provided by a MRC
            project grant. The DNA was prepared from embryos by Alain Bucheton
            and Genevieve Payan. It has been constructed in the vector
            pBeloBAC11.
FEATURES   Location/Qualifiers
     source   1. .1025
                     /organism="Drosophila melanogaster"
                     /plasmid="pBeloBAC11"
                     /db_xref="taxon:7227"
                     /clone_lib="DrosBAC"
                     /clone="BACN11l11"
                     /note="end : T7"
BASE COUNT   148 a   88 c   6 g   522 t   261 others
ORIGIN

Query Match   1.4%;   Score 53;   DB 121;   Length 1025;
Best Local Similarity   33.0%;   Pred. No. 0.057;
Matches   223; Conservative 68; Mismatches 384;   Indels   0;   Gaps   0;

Qy   226 aaaaaacgataccgtgatgcgtagacattagtgataaaagacaggtgtgcgcgaaaaagac 285
              ||||| || | | | || | || || ||| | |:||
Db   794 AAAAAAKAAAAGKTGCAAAAAAKRTTRTRTTRTRGTGTTAAAAAATATGTRTGRTARWATAA 735

Qy   286 gcttacttagctgattacaaaagaatatgaaacttacgtttcaaagcaaacccctaa 345
              ||-| |: || | | :|| || |||
Db   734 WAATRTRKKKTGATGRTRAARAWAWWAAAATATAAATAWAYGAAKTGRAAAAAAARAAAAA 675

Qy   346 tctggcgaagctcgtgctagcaacttacatcgatgtcttacaacctatgcaacaaaattagac 405
              | :| || | || | || | | || | ||
Db   674 ATGTRAWAWATRAWATTRKKATTGTGAATWKGTTKGTRKKAWAAAAAWAKWRWT 615

Qy   406 gaaatgcgcccaagacgaggctgctgttcaagcaaaagatttagaaaagcagaacaa 465
              : :| || | || | | |:|||| | | ||
Db   614 AAWKKTARAAWDGTKKKTWKTKTTTRAAWAAKGGRGTGKGKAKGTTRRDWWAAAAAAAA 555

Qy   466 tactatcacaaaattcctatgaaattaaaactcgacacagtcattagatcgcgtatat 525
              || | | | | | :|||: |||| | |
Db   554 AAAAAAAKAAAAGGGTGAADARAAKGDAAARADAGRWAAAARAKRFATAKRGTGKIRTK 495

Qy   526 ggtaaacaactcgtgattacttcgcctctacatttaaagcaaagcacaagaacttcgc 585
              | | | || | | | ||| | | || | |:| | | ||
Db   494 TGTKTAGTKATRAAGAKTWAAATWAAAAAGTTGTKAKWAATATTRAAAAAAAAAAKWRTG 435

Qy   586 gacagcttaatttatataccgttgcaatgaaagcgcgcgaagtacaagacgcgtg 645
              |: | || |||| :|||| | :|: | |||| :| |
Db   434 GRTGKRGAGAAITTATRTAKKTTAAAAWAAGTGTKAKWANTATTRAAAAAAAKRTGKTGDKAARAAADAAAT 375

Qy   646 aaagcacggcaatttagacaaagctaaagctgctgttgatcaaatcaatacttacca 705
              |: |||||| ||| ||| | | | ||||||
Db   374 TAAAAAAAGAAGAAAAAAAAAAAAANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 315

Qy   706 aaagtaacagttgcttcaaaactgaactaacagaagctagcgaaaaagcattagatgca 765
              ||| ||| || | | ||| | |||||||| || |
Db   314 AAAAAAAAAAGAAAAAAAAAAAAAAAAANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 255

Qy   766 gatgaagctcgcgcttactccaaaagttgaaagtgaagttgcgaattaacactcaaaacaa 825
              || | || | || ||| | ||
Db   254 AAAAAAAAAAAAAAAAAAAAAAAAAAAAANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 195

Qy   826 gctgtgaattaacagcagtaccagtgaacggaacactaaaattacaacttcagctgct 885
              || || | |||| ||| | || | | ||||||
Db   194 AAAAAAAAAAAAAAAAAAAAAAAANNNNNNNNNNNNNNNANNGNANNNNNAAANNNNNA 135

QY   886 gcaaatgaagataca 900
              ||| | | |

Db   134 AAAAANNNANANNNA 120

RESULT 11

B13042/c

LOCUS   B13042   1147 bp   DNA   GSS   14-MAY-1997
DEFINITION   T30M24-Sp6.1 TAMU Arabidopsis thaliana genomic clone T30M24, DNA
    sequence.
ACCESSION   B13042
VERSION   B13042.1   GI:2094174
KEYWORDS   GSS.
SOURCE   thale cress.
  ORGANISM   Arabidopsis thaliana
    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
    Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
    Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 1147)
  AUTHORS   Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
    Ecker,J.
  TITLE   BAC End Sequences at ATGC
  JOURNAL   Unpublished (1997)
COMMENT   Other_GSSs: T30M24-Sp6, T30M24-Sp6.2
    Contact: Ecker J.
    Arabidopsis Thaliana Genome Center
    University of Pennsylvania
    Dept. of Biology, University of Pennsylvania, Philadelphia, PA
    19104
    Tel: 215-898-9384
    Fax: 215-898-8780
    Email: jecker@atgenome.bio.upenn.edu
    Seq primer: Sp6
    Class: BAC ends
    High quality sequence start: 289
    High quality sequence stop: 292.
FEATURES   Location/Qualifiers
    source   1..1147
    /organism="Arabidopsis thaliana"
    /strain="Columbia"
    /db_xref="taxon:3702"
    /clone="T30M24"
    /clone_lib="TAMU"
    /sex="hermaphrodite"
    /note="Vector: BeloBACII; Site_1: HindIII; Site_2: HindIII
    ; Produced by Rod Wing"
BASE COUNT   3 a   4 c   46 g   553 t   541 others
ORIGIN

Query Match   1.4%;   Score 53;   DB 118;   Length 1147;
Best Local Similarity   26.1%;   Pred. No. 0.059;
Matches 212;   Conservative   0;   Mismatches 600;   Indels   0;   Gaps   0;

Qy   94 acagatgtagcaacagtgtaagcaagcaacagttcaaaaagcatactatact 153
          | ||| | | ||||| | ||||| |||||||| ||||||
Db   1100 ANNAAAANANANNAAAAAAAAANctggtgattccaaacttaacgatgtatatgctgaa 1041

Qy   154 tacagcccatacagtaacggaaactggtgattccaaacttaacgatgtatatgctgaa 213
          |||| ||| | ||||| |||| |||||||||||||||||||||||||||||||||||||
Db   1040 AAAAANANANNANAAAAAAANANNANANAAANNNAAAAAAAANNNNANNNNNAAAAAAAN 981

Qy   214 tacaacaaagcgaaaaacgataccgtgatgcggtagcacttagtgaataaagcaggtggc 273
          || || |||| ||||||||||| ||||||||||||||||||||||||||||||| |||||
Db   980 ANNAANNANNAANANANNANNNANNAAAAAAANAAAAAAAAANNANANANNNNNNNN 921

Qy   274 gcggaaaaagcacgcttacttagctgattcacaaaaagaatatgaaacttacgttttcaaa 333
          ||| |||||| |||||||||||| ||||||||||| ||| |||
Db   920 AAAANNAANAAANANANAAAAAAANANAAAAAAAAAAANANNANNNAAAAAAAAAAA 861

Qy   334 gcaaacccctaaactcggcgaagctcgtgtcgtgtcaacttacactcgatgctcacactatgca 393
          ||| ||||||||| |||||||||||||||||||||||||||||||||||| ||| ||||
Db   860 AAANANANNNANANAAAAANANNAAAAAANANNNNNAAAANAAANAAAAAAAAAA 801

Qy   394 acaaaattagacgaaatcgccaagaagctgaggcgctgctgttcaagcaaaaagatttagaa 453
          ||| |||||||||||||||||||||||||||||||||||||

Db   800 AAAAAANNNANANNNAAAAAAAAAAAAAAAAAAAAAAAANNAAAAAAAAAAANANANAAAAA 741
          | ||| | || |||| ||| |
Qy   454 aaagcagaacaatactacataAANAAAAatcctatgaaattaaaactgcacagtcattta 513

Db   740 AAAAAAAAAAAAAANNNAANAAAAAANAAAAAAAAAAAAANANANNAAANAAAAANNNN 681
          ||||||||||||||| || | |||||||||||||||||| ||||| | | ||
Qy   514 gatcgcgtatggtaaacaactcgtgattacttcgctcacattaaagcaaagca 573

Db   680 NAAAAANAAAAAANAAAAAAAAAAAAAANNAANNNNNANAAAAAAANANANNAAAANANA 621
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   574 caagaacttcgcacagctaatttatgatattaccgttgcaatgaaagcgcgcgaagta 633

Db   620 ANAAANNANANANAAANNAANANNNNANNANAAAAAAAAANNNNNNANNNNNNNNNNNNNN 561
          | ||| | | ||||| |||||
Qy   634 caagagcgctgtgaagcaggcaatttagacaaagctaaagctgctgttgatcaaatcaat 693

Db   560 NNNNNNNANNAAAAAAAANAAAAANANNANNNNNNNNNNNNNNNNNNNNNNANNAAAAAA 501
          ||||||| |||||||| ||||| | ||
Qy   694 caatacttaccaaaagtaacagatgctttcaaaaactgaactaacagaagtagcgagaaa 753

Db   500 AAAAAAAANANANAAAAAAAAAANNNNNANNNNNANAAANNANNNNNNAAAAAAAAAA 441
          |||||||| | || | ||||||||||| | ||||| | || |||||
Qy   754 gcattagatgcaagatgaagctcgcgcttacctccaaaagttgaaagtgtaagtcgattaac 813

Db   440 AAAAAAAAAAAAAANNAAAANNNANAAAAAANNNAANAAAAAAAAAANANNNNNAAAAA 381
          |||||||||||||| ||| | |||||| || ||||||||||| | |||
Qy   814 actcaaaacaaagctgttgaattaacacagtaccagtgacggaacctaaaattcaa 873

Db   380 ANAAAAAAAAAAAAAAAAANNNAANNAANANANNNANANAANAAAAAANNNNAAAANNN 321
          ||||||||||||||||||| || || | ||| | ||| ||||| ||| || |
Qy   874 ctttcagctgctgcaaatgaagatacagtaa 905

Db   320 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAAAAAAA 289
          | |||
Qy   874 ctttcagctgctgcaaatgaagatacagtaa 905

RESULT 12

CNS00655

LOCUS   CNS00655   959 bp   DNA   GSS   03-JUN-1999
DEFINITION   Drosophila melanogaster genome survey sequence TET3 end of BAC #
    BACR13F18 of RPCI-98 library from Drosophila melanogaster (fruit
    fly), genomic survey sequence.
ACCESSION   AL062806
VERSION   AL062806.1   GI:4943996
KEYWORDS   GSS.
SOURCE   fruit fly.
  ORGANISM   Drosophila melanogaster
    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
    Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
    Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 959)
  AUTHORS   Genoscope.
  TITLE   Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
    BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
    - Web : www.genoscope.cns.fr)
COMMENT   Determination of this BAC-end sequence was carried out as part of a
    collaboration with the Berkeley Drosophila Genome Project (BDGP).
    The BDGP is constructing a physical map of the Drosophila
    melanogaster genome using these BACs. For further information
    please see http://www.fruitfly.org The BDGP Drosophila
    melanogaster BAC library was prepared by Kazutoyo Osoegawa and
    Aaron Mammoser in Pieter de Jong's laboratory in the Department of
    Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
    NY. The library is named RPCI-98 and was constructed by partial
    EcoRI digestion of Drosophila DNA provided by the BDGP from the
    isogenic strain y2; cn bw sp, the same strain used for the BDGP's
    P1 and EST libraries. A more detailed description of the library
    and how to order individual BAC clones, the entire library, or
    filters for hybridization from the BACPAC Resource Center can be
    found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES   Location/Qualifiers
    source   1..959

RESULT 13

LOCUS	CNS00IDL 969 bp DNA GSS 03-JUN-1999	
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC:	
	BACR35C06 of RPCI-98 library from Drosophila melanogaster (fruit	
	fly), genomic survey sequence.	
ACCESSION	AL074848	
VERSION	AL074848.1 GI:4954426	
KEYWORDS	GSS.	
SOURCE	fruit fly.	
ORGANISM	Drosophila melanogaster	
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;	
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
REFERENCE	1 (bases 1 to 969)	
AUTHORS	Genoscope.	
TITLE	Direct Submission	
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :	
	BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)	
	- Web : www.genoscope.cns.fr)	
COMMENT	Determination of this BAC-end sequence was carried out as part of a	
	collaboration with the Berkeley Drosophila Genome Project (BDGP).	
	The BDGP is constructing a physical map of the Drosophila	

Query Match   1.4%;   Score 51.8;   DB 121;   Length 959;
Best Local Similarity   32.8%;   Pred. No. 0.11;
Matches 167;   Conservative   80;   Mismatches 262;   Indels   0;   Gaps   0;

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Qy   437 aagcaaaagatttagaaaaagcagaacaatactatcacacaaattccttatgaaattaaaa 496
              |||||| |:|| ||| : ||:| |||: | |||  | ||| |||||  ||||
Db   293 AAAAAAAAAMMMAAAAAAMMMCMAACACAAYMAAAAAMCACAAYMAAAAAAAAAAAAA 352

Qy   497 ctcgcacagtcattttagatcggtatatgtaaaacaactcgtgattacttcgctcta 556
              : |:|:  ||| ::|||| |: ||| ||||  ||| ||| |||||||||||||
Db   353 CAACYANAWYTAAAAAAACACSGCSSMYMAWWMMMMCSMAASRTTSRTTSCCWMTCCCC 412

Qy   557 catttaaagcaaaagcacaacaaacttcgcgacagcttaattatgatattaccgttgcaa 616
              |:::| ||||||  ||||||||: ||||:||::||| |||||  ||||| |||:||||
Db   413 CCCMCCCCSARRAARAARAAAASTTTRYRTTGDGMKTKTKTWATTGKAATAWGARAAGAAA 472

Qy   617 tgaaagcgcgcgaagtacacagacgctgtgaaagccaattagaaccaaagctaaagctg 676
              :|:|| : |  |||: :|||  :| ||||| ||| |||| |||| ::|| ||||:
Db   473 GRAKARARGARAAAAAAADAARAAAAAAKBGTAKRTWAAGGRAAKTRAG 532

Qy   677 ctgttgatcaatcaatctattaccaaaaagtaacgatgctcttcaaaaactgaactaa 736
              : |||| |||||  ||||||||   |||:| |: :|||||||||:|| |||
Db   533 GRAAAARWAKDAAAARGGGAARAAAAAANTTAAAAAAAATDAAAAAA 592

Qy   737 cagaagtagtcgcaaaaagacattagatgcagatgaagctgcgcttactccaaaagtgaa 796
              |||| |||||||||||||||||:|||:|||| |||  |||| ::||| :|:
Db   593 KAWAAAAAAAAAAAAAAGAAWAWRAAKDAAAAAADAGGGKAAARTATATKAAWAK 652

Qy   797 gtgtaagtgcgattaacactcaaaacaaagctgttgaattaacacagtaccagtgaacg 856
              |:|| ||  ||||||||||||||||: |||:| ||||||:|||||||| ||||:| :
Db   653 AATATAAAAWWTTRTTTWAWTTWAKRAAAAAAAAAAAAAAATARDMDAWAWAWAARRAA 712

Qy   857 gaacaactacacactttcagctgctgcatagcaagtaaacgtaaatactg 916
              ||||||| ||| :||||| ||||||:||:| |||||: |:||| ||||
Db   713 AAAAAADRAAARAAAAAWADGRKAAAAAAAAWRAAKAIKRDGAWWAAAAAAA 772

Qy   917 tacgtatcctataaagtggacggtaacatt 945
              |||:| : ||:|||  |||||:|
Db   773 AADGDARGDTDAAWAAARKKGDAAAAWTT 801
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FEATURES	Location/Qualifiers	
source	1..969	
	/organism="Drosophila melanogaster"	
	/db_xref="taxon:7227"	
	/clone_lib="RPCI-98"	
	/clone="BACR35C06"	
	/note="end : TET3"	

BASE COUNT   502 a   133 c   93 g   150 t   91 others
ORIGIN

RESULT 14

LOCUS	CNS00HX9 1101 bp DNA GSS 03-JUN-1999	
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC:	
	BACR35M04 of RPCI-98 library from Drosophila melanogaster (fruit	
	fly), genomic survey sequence.	
ACCESSION	AL073856	
VERSION	AL073856.1 GI:4953838	
KEYWORDS	GSS.	
SOURCE	fruit fly.	
ORGANISM	Drosophila melanogaster	
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;	
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
REFERENCE	1 (bases 1 to 1101)	
AUTHORS	Genoscope.	
TITLE	Direct Submission	

Query Match   1.4%;   Score 51.8;   DB 121;   Length 969;
Best Local Similarity   40.5%;   Pred. No. 0.11;
Matches 158;   Conservative   27;   Mismatches 205;   Indels   0;   Gaps   0;

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Qy   190 aacattaacgtatgtatatgctgaatacacaaagcgaaaaaagataccgtgatgtcggta 249
              |||||   |:| |||||||  |||||||||:|| |||||||||| |||| ||| |||
Db    43 AACARAAAAAAACANNAGAAAAAAGAAAAAAAAARAAATAARAACACCAAAAAGAAAAAACA 102

Qy   250 gcattagtgaataaagcaggtggcgcgaaaaagacgcttacttagctgatttacaaaaa 309
              ||| |:|||||||  ||||| ||:|| ||||||| |||:| ||||:||||||:||
Db   103 CAACCGGAAAWAMAAACGCWTWAWACAAWAAACAAAAAGAAAAAAWCGRAAMCAAAAAMA 162

Qy   310 gaatatgtaaacttacgtttcaaagcaaacccctaaaatctggcgaagctcgtgtagcaact 369
              ||| |||  ||||| |||||||:||| |||  ||||||||  |:|||| |:| |||| |
Db   163 CAAAAMAAAAMCAAAAAAAMCAAAAAAAACRCACCAAAAAAAGGAAAAGTTCAAMAAAAAAA 222

Qy   370 tacaatcgtgtctacaactatgcaacaacaaattagacgaaatgtggccaagacgtaagagc 429
              ||| |:|||: ||||||| |||||||||||:||||||| |::|| |||||:||||||| ||
Db   223 AAAAAAARCGCMCRAAAAAATCRAAMAAAGRAAAAAAAACRAAMGGGCGAAAAAAA 282

Qy   430 gctgttcaagcaaaagatttagaaaaagcagaacaatactatcacaaaattcctatgaa 489
              |||:||||  ::||||| ||||||||||| | ||| |||||||: ||||||| |||||
Db   283 MACACACAAAMAAAAAAAAAMAAAAAACAAAAAAARTGTWAAMRAAAAAAAGCA 342

Qy   490 attaaaactcgtacagtcatttagatcggtatatggtaaaacaaactcgtgattactt 549
              |||||:|  :|||| ||  |||||||||  |||||| |||| |:||| |||||| ||||
Db   343 AAAAAAARATGCAAAAAATGCTTAAAGCAGGAAAAAAAAAAAAAAAAAAAAAAAAAAA 402

Qy   550 cgctcctacatttaaagcaaaagcacaagaa 579
              ||  |:|||||||||||| ||||  |||||
Db   403 GCCGAAAAAAAAMAAAAAAAAAAAAAAMA 432
```

JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)

COMMENT   Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain Y2; cn bw sp; the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES   Location/Qualifiers
        source   1..1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clone="BACR35M04"
                     /note="end : TE13"

BASE COUNT   164 a   100 c   120 g   616 t   101 others
ORIGIN

Query Match   1.4%;   Score 51.8;   DB 121;   Length 1101;
Best Local Similarity   40.1%;   Pred. No. 0.11;
Matches 241;   Conservative 32;   Mismatches 324;   Indels   4;   Gaps   1;

Qy   258 gaataaagcaggtggcgcgaaaaagaacgcttacttagctgatttacacaaagaaatga 317
                ||| || | ||||||||| |||| |||||:|
Db   618 GAACTAAAGACGAGGATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTAAAA 559

Qy   318 aacttacgtttcaaagcaaacctaaatctgtcgvaagctcgtcgtagcaacttacatcga 377
                || | || |:: || ||| ||
Db   558 AAATAAAAAATAAAAAATWAAAAAAGTGAAAAAARAWAAAAAAAAAAAAAAAA 499

Qy   378 tgcttacaactatgcaacaaaattagcacgaaatcgccaaagagcgctagagcgtgttca 437
                || ||| | || | |||| |||| |||| ||
Db   498 AAAATAARTAAAAAAAAAAATTAAAAAAAAAAAWAAAAAAAAAAACTGAAA 439

Qy   438 agcaaaagattagaaaaaagcaggaacaatactatcacaaaatcccttatgaaatgagtga 497
                ||||||| | |||| ||| | || ||||| | |||: |||: |||
Db   438 TGTAAGAAAAWAAAAAWAAAAATAAAAAAAAAARRGTAGAAAAAATTAAA 379

Qy   498 tcgcacagtcatttagatcggcgtatatggtaaaacaactcgtgattacttcgctctac 557
                | ||| | || || | || |||| ||| ||
Db   378 ----AAAAWAAAAATAAWAAAAAAAAAAAGWAAAAAAAAAAAAAWAA 323

Qy   558 atttaaagcaacaagaacttcgcgacagctaatttatgatattaccgttgcaat 617
                || ||| |: |:
Db   322 AAAAAATAATAAAAWAAAAAWAAAAWAAWWAAAARRAAAAWWWAAAAAWAAAAAA 263

Qy   618 gaaagccgcgaagtacaagagctgtgaaagccaaattagacaaagctaaagctgc 677
                | ||||| ||: |||||| |||||| |||| | | ||||||
Db   262 AAAAATAACAAAAAWAAAWAATARAAAAAWAAATAAAAWWAAAAAWAAAAACAAT 203

Qy   678 tgttgatcaaatcaatacttaccaaaagtaacagatgcttcaaaactgaactaac 737
                |||| | ||:|| || | | | | | |||: | |:|
Db   202 TWTAAAAAAWAAAAACTTWAAWAAWATWAAAAAAACCCAGAAATT 143

Qy   738 agaagtagcgaaaaagcattagatcgagatgaagctgcgcttacctccaaagtgaag 797
                |||| | |||| | | || | || |||| ||
Db   142 AATAAGWAAWGAGAAAAAAAAAATAAAATAAWAMAAAAAAAAAAAAWAW 83

Qy   798 tgtaagtcgcgattaaacactcaaaacaagctgttgattaacagcaagtaccagtgaacgg 857
                || | ||||| |:|| ||| ||: |||||||| ||||||||||||||||||||||
Db   82 TAAIATTICATAAAWAAGAGAAWAAAAAAATTWAAATATTAAAATACAAGAACCGG 23

Qy   858 a 858
           |
Db   22 A 22

RESULT 15

LOCUS   FR0018463   470 bp   DNA   GSS   09-DEC-1997
DEFINITION FR0018463/c
            F:rubripes GSS sequence, clone 016E10aC6, genomic survey sequence.
ACCESSION   AL011359
VERSION   AL011359.1 GI:2676793
KEYWORDS   GSS; genome survey sequence.
SOURCE   Fugu rubripes.
ORGANISM   Fugu rubripes
            Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii;
            Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
REFERENCE   1 (bases 1 to 470)
AUTHORS   Elgar,G.; Clark,M.; Smith,S.; Meek,S.; Warner,S., Umrania,Y.,
            Williams,G. and Brenner,S.
TITLE   Direct Submission
JOURNAL   Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
            Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
COMMENT   Vector: pBluescript II KS
            V_type: phagemid
            PRIMER: KS
            DESCR:
            One pass dye-terminator sequencing of cosmid cloned genomic
            sequence.

FEATURES   Location/Qualifiers
        source   1..470
                     /organism="Fugu rubripes"
                     /db_xref="taxon:31033"
                     /clone_lib="cosmid 016E10"
                     /clone="016E10aC6"

BASE COUNT   149 a   150 g   65 t   27 others
ORIGIN

Query Match   1.4%;   Score 51.6;   DB 124;   Length 470;
Best Local Similarity   44.9%;   Pred. No. 0.1;
Matches 159;   Conservative   0;   Mismatches 195;   Indels   0;   Gaps   0;

Qy   1264 gttactattacagatgttgaaactggaaaacgcattccagtaattgcatcctactctggt 1323
                ||| | | || | || || ||| | || || | |||| | |
Db   396 GCTGCTACTACTGGTGCTACTACTGCTACTGCTACTACTNCTGCTACTAATGCTGCT 337

Qy   1324 tctacaattactattacgttaaaagaagcgttagtaactggtaaacaatataaacttgct 1383
                | | || | || | || || || | |||| | || | || || ||
Db   336 GCTACTACTGGTGCTACTGCTACTGCTACTACTGCTACTGCTACTGCT 277

Qy   1384 atcaataatgttaaaacattaactggttacaatgcagaagcttacgagttagttcact 1443
                | | | || || || || || | || || | | || || || || | |
Db   276 GCTACTGCTACTGCTGCTACTGCTACTACTGCCTINCTNAAINCTGCTACTGCTNCT 217

Qy   1444 gcaaacgcatcagcaccaactgttgctaccgctcctactacttaggtggttacaactta 1503
                |||| || | | |||||| | || || |||| || || |||||||| |||
Db   216 NCTNCTGCTACTACTGCTACTACTGCTACTGCTGCTGCTGCTGCTACTGCTGCT 157

Qy   1504 tctactggttctcttacacacaaatgtttgggtaaattggctggtggtgtgaatgaagct 1563
                | | ||||| | | | ||| | | || ||||| | |||| || || | | |||
Db   156 GCTGCTACTACTGCTACTGCTACTACTGCTCGTGCTGCTGCTACTACTGCTACT 97

Qy   1564 ggaacttattatcctgggtcttcaattcacacaacaacgtttgctactaagttagac 1617
                || || || | || | | |||| | | ||| | ||| | || || || | ||
Db   96 ACTGCTGCTGCTGCCTACTGCTGCTCTNNTANCCCTNCTNCTNCNGCTCGCNTANTNCTAC 43

Search completed: December 9, 2000, 11:59:36
Job time: 7346 sec

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